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Reviewer: Durreshwar Anjum

Timestamp: Wed Oct 10 10:22:36 EDT 2007

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Application No: 10580142 Version No: 1.0

**Input Set:**

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**No. of SeqIDs Defined:** 14  
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## SEQUENCE LISTING

<110> Aventis Pasteur Limited  
Brunham, Robert  
Raudonikiene, Ausra  
Gallichan, Scott  
Murdin, Andrew

<120> Immunization Against Chlamydia Infection

<130> APL-03-03-PCT-US

<140> 10580142  
<141> 2007-09-24

<150> PCT/CA2004/002001  
<151> 2004-11-19

<150> 60/481,690  
<151> 2003-11-21

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Ser Ala Ser Cys Asp Phe Pro Pro Ser Val Ser Gln Lys Ile Leu Phe  
20                   25                   30

ttg tgt caa aaa tct att cct caa gct ctg gag tcc tat ctt gag gca       144  
Leu Cys Gln Lys Ser Ile Pro Gln Ala Leu Glu Ser Tyr Leu Glu Ala  
35                   40                   45

tct aca acc tat caa caa cat aac ttt tct ata ttg cgc tta ata gct       192  
Ser Thr Thr Tyr Gln Gln His Asn Phe Ser Ile Leu Arg Leu Ile Ala  
50                   55                   60

aag tca tac tta caa caa agt ctc ttt tct gaa gat gct tac gta cgc       240  
Lys Ser Tyr Leu Gln Gln Ser Leu Phe Ser Glu Asp Ala Tyr Val Arg  
65                   70                   75                   80

aaa agc gca att att gga gcg ggg ctt tct ggc tca tct gag act cta Lys Ser Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Thr Leu	85	90	95	288	
gat cta ctg tct gaa tcc ata gaa aca cag gat ctt tat gag cag cta Asp Leu Leu Ser Glu Ser Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu	100	105	110	336	
ctt att tta aat gct gca ggc aat caa tta ggc aaa act tcc gat cgt Leu Ile Leu Asn Ala Ala Gly Asn Gln Leu Gly Lys Thr Ser Asp Arg	115	120	125	384	
ctt tta ttc aaa gga tta aca gca cct cat cct att att cgc ttg gaa Leu Leu Phe Lys Gly Leu Thr Ala Pro His Pro Ile Ile Arg Leu Glu	130	135	140	432	
gct gct tac cgt ctg gcc tgt atg aaa aac agt aaa gta agt gac tac Ala Ala Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr	145	150	155	160	480
ctc tat tct ttt atc cac cag ctt cca gaa gaa atc caa aac tta gca Leu Tyr Ser Phe Ile His Gln Leu Pro Glu Glu Ile Gln Asn Leu Ala	165	170	175	528	
gca acg att ttt ttg cag ctc gaa acg gaa gaa gca gat gct tat gtt Ala Thr Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Val	180	185	190	576	
cat aga ctc ctg tct tct cct aat agt cta aca aga aac tat atg gct His Arg Leu Leu Ser Ser Pro Asn Ser Leu Thr Arg Asn Tyr Met Ala	195	200	205	624	
tat cta att gga gaa tat caa cag agg aga ttt ctt cca acg ctc cgc Tyr Leu Ile Gly Glu Tyr Gln Gln Arg Arg Phe Leu Pro Thr Leu Arg	210	215	220	672	
tcg ttg ctt acc agc gca gct cct tta gac caa gaa gga tct ttg tat Ser Leu Leu Thr Ser Ala Ala Pro Leu Asp Gln Glu Gly Ser Leu Tyr	225	230	235	240	720
gct ata gga aaa tta gaa gat gcc agc agc tat cct aaa atc aaa gca Ala Ile Gly Lys Leu Glu Asp Ala Ser Ser Tyr Pro Lys Ile Lys Ala	245	250	255	768	
tta agc tcc aaa tct aac cct gaa gtg gct ctt gct gct gct cag aca Leu Ser Ser Lys Ser Asn Pro Glu Val Ala Leu Ala Ala Gln Thr	260	265	270	816	
tta tta ttc ttg ggt aaa gaa gat gag gct ctt cct atc cta act act Leu Leu Phe Leu Gly Lys Glu Asp Ala Leu Pro Ile Leu Thr Thr	275	280	285	864	
ttt tgc cag caa gag ctt cct cga gct att tat acc tct cgt ttc ctt Phe Cys Gln Gln Glu Leu Pro Arg Ala Ile Tyr Thr Ser Arg Phe Leu	290	295	300	912	
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305	310	315	320
att aaa gaa gaa att aaa ctg aat gct gct ttg gct ctt gtc cac ttg			1008
Ile Lys Glu Glu Ile Lys Leu Asn Ala Ala Leu Ala Leu Val His Leu			
325	330	335	
gga agc gtt aat cac cta gtg ctt agt tat tta aca gaa ttt tta gaa			1056
Gly Ser Val Asn His Leu Val Leu Ser Tyr Leu Thr Glu Phe Leu Glu			
340	345	350	
aat aaa att ctc cac cgc ata ttt tta ccc acc cat tcg ata gga aaa			1104
Asn Lys Ile Leu His Arg Ile Phe Leu Pro Thr His Ser Ile Gly Lys			
355	360	365	
gcc acg cag ttt tgg aaa gag tgt acg gca ctc cct ctt cta agc cca			1152
Ala Thr Gln Phe Trp Lys Glu Cys Thr Ala Leu Pro Leu Leu Ser Pro			
370	375	380	
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Glu Glu Lys Ala Arg Ala Leu Ala Met Tyr Arg Ala Ala Glu Asp Thr			
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Ile Leu Ser Ser Leu Leu Lys Leu Pro Asn Asn Ala Tyr Leu Pro Tyr			
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ttg gaa cgt att cta act tca caa aaa acc cct cta gca gct aaa gct			1296
Leu Glu Arg Ile Leu Thr Ser Gln Lys Thr Pro Leu Ala Ala Lys Ala			
420	425	430	
att gct ttt tta tca gta aca gct cat cct cag gca ctt tct tta gtc			1344
Ile Ala Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val			
435	440	445	
tcg aaa gca gca cta act cca gga gac cct atc att cgc gct tat gcg			1392
Ser Lys Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala			
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aat tta gct tta tat aca atg acg caa gat cct gaa aag aaa gcc tta			1440
Asn Leu Ala Leu Tyr Thr Met Thr Gln Asp Pro Glu Lys Lys Ala Leu			
465	470	475	480
tta tat caa tat gcc gaa cag tta ata gga gac acg att ttg ttt aca			1488
Leu Tyr Gln Tyr Ala Glu Gln Leu Ile Gly Asp Thr Ile Leu Phe Thr			
485	490	495	
gat gag gag aat ccc ctg cct tct ccc cat tct tcc tac ctg cga tat			1536
Asp Glu Glu Asn Pro Leu Pro Ser Pro His Ser Ser Tyr Leu Arg Tyr			
500	505	510	
caa gtg tcc cca gaa act cgt tct caa ctc atg cta act att tta gaa			1584
Gln Val Ser Pro Glu Thr Arg Ser Gln Leu Met Leu Thr Ile Leu Glu			
515	520	525	
acc cta gtt tct tct aaa act gat gaa gac atc cga gtt ttt ctt tcg			1632
Thr Leu Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser			

530

535

540

cta atg aaa aaa acc cat tac aaa aat atc ccc atc tta tct gga tta  
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1698

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Leu Cys Gln Lys Ser Ile Pro Gln Ala Leu Glu Ser Tyr Leu Glu Ala  
35 40 45

Ser Thr Thr Tyr Gln Gln His Asn Phe Ser Ile Leu Arg Leu Ile Ala  
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Lys Ser Tyr Leu Gln Gln Ser Leu Phe Ser Glu Asp Ala Tyr Val Arg  
65 70 75 80

Lys Ser Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Thr Leu  
85 90 95

Asp Leu Leu Ser Glu Ser Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu  
100 105 110

Leu Ile Leu Asn Ala Ala Gly Asn Gln Leu Gly Lys Thr Ser Asp Arg  
115 120 125

Leu Leu Phe Lys Gly Leu Thr Ala Pro His Pro Ile Ile Arg Leu Glu  
130 135 140

Ala Ala Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr  
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Leu Tyr Ser Phe Ile His Gln Leu Pro Glu Glu Ile Gln Asn Leu Ala  
165 170 175

Ala Thr Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Val  
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His Arg Leu Leu Ser Ser Pro Asn Ser Leu Thr Arg Asn Tyr Met Ala  
195 200 205

Tyr Leu Ile Gly Glu Tyr Gln Gln Arg Arg Phe Leu Pro Thr Leu Arg  
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Ala Ile Gly Lys Leu Glu Asp Ala Ser Ser Tyr Pro Lys Ile Lys Ala  
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Phe Cys Gln Gln Glu Leu Pro Arg Ala Ile Tyr Thr Ser Arg Phe Leu  
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Ser Leu Glu Lys Gly Glu Glu Leu Leu Pro Ile Phe Cys Lys Ala  
305 310 315 320

Ile Lys Glu Glu Ile Lys Leu Asn Ala Ala Leu Ala Leu Val His Leu  
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Gly Ser Val Asn His Leu Val Leu Ser Tyr Leu Thr Glu Phe Leu Glu  
340 345 350

Asn Lys Ile Leu His Arg Ile Phe Leu Pro Thr His Ser Ile Gly Lys  
355 360 365

Ala Thr Gln Phe Trp Lys Glu Cys Thr Ala Leu Pro Leu Leu Ser Pro  
370 375 380

Glu Glu Lys Ala Arg Ala Leu Ala Met Tyr Arg Ala Ala Glu Asp Thr  
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Leu Glu Arg Ile Leu Thr Ser Gln Lys Thr Pro Leu Ala Ala Lys Ala  
420 425 430

Ile Ala Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val  
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Ser Lys Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala  
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Leu Tyr Gln Tyr Ala Glu Gln Leu Ile Gly Asp Thr Ile Leu Phe Thr  
485 490 495

Asp Glu Glu Asn Pro Leu Pro Ser Pro His Ser Ser Tyr Leu Arg Tyr  
500 505 510

Gln Val Ser Pro Glu Thr Arg Ser Gln Leu Met Leu Thr Ile Leu Glu  
515 520 525

Thr Leu Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser  
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Ser Ala Ser Cys Asp Phe Pro Ser Ser Val Ser Gln Arg Ile Leu Phe  
20                  25                  30

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Ser Cys Arg Lys Ser Val Pro Gln Ala Leu Glu Ala Tyr Leu Glu Ala  
35                  40                  45

tca gca act tat caa caa cac gat ttc tcc gta tta cgc gta ata gca      192  
Ser Ala Thr Tyr Gln Gln His Asp Phe Ser Val Leu Arg Val Ile Ala  
50                  55                  60

gaa tcg tat tta caa caa agc ttt ctc tct gag gac acc tac ata cgt      240  
Glu Ser Tyr Leu Gln Gln Ser Phe Leu Ser Glu Asp Thr Tyr Ile Arg  
65                  70                  75                  80

aaa agt gca att att gga gca ggg cta tct ggt tca tca gaa gct tta      288  
Lys Ser Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Ala Leu  
85                  90                  95

gag tta ctg tct gag gct ata gaa acg caa gat ctc tat gag caa cta      336  
Glu Leu Leu Ser Glu Ala Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu  
100                105                110

ctc att tta aat gct gca acc agc caa tta agc aaa act tct gac aaa      384  
Leu Ile Leu Asn Ala Ala Thr Ser Gln Leu Ser Lys Thr Ser Asp Lys  
115                120                125

ctt tta ttc aag gga tta aca gct tct cat cct gtc atc cgc tta gaa      432  
Leu Leu Phe Lys Gly Leu Thr Ala Ser His Pro Val Ile Arg Leu Glu  
130                135                140

gct gct tat cgt ctt gcc tgt atg aaa aat agc aag gta agt gat tac      480  
Ala Ala Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr  
145                150                155                160

ctt tat tct ttt atc tac aag tta cca gaa gaa att caa aac cta gcg      528  
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165                170                175

gca act att ttc tta caa ctc gaa aca gaa gaa gct gat gct tat att      576  
Ala Thr Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Ile  
180                185                190

cat cat ttg ctc tct ccc aat aac ctg aca aga aac tat gtt gcc        624  
His His Leu Leu Ser Ser Pro Asn Asn Leu Thr Arg Asn Tyr Val Ala  
195                200                205

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240		
gcg tta ggc aaa ctg gaa gac tct ggt agc tat cct aga att aaa gct		768
Ala Leu Gly Lys Leu Glu Asp Ser Gly Ser Tyr Pro Arg Ile Lys Ala		
245	250	255
cta agc tct aga tcc aat cct gaa gta gta ctc gct gca gct cag aca		816
Leu Ser Ser Arg Ser Asn Pro Glu Val Val Leu Ala Ala Ala Gln Thr		
260	265	270
tta tta ttc tta gag aaa gaa gaa gaa gct cta ccg atc cta acc aac		864
Leu Leu Phe Leu Glu Lys Glu Glu Ala Leu Pro Ile Leu Thr Asn		
275	280	285
ctt tgc caa caa aaa ctt ctt cga gcc ctg tat acc gca cgt ttc ctc		912
Leu Cys Gln Gln Lys Leu Leu Arg Ala Leu Tyr Thr Ala Arg Phe Leu		
290	295	